

FIGURE 1A.

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC  
51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA  
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC  
151 TACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA  
201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC  
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC  
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTGGC  
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT  
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG  
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC  
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TCGGGCTCAA ATGGAAGAGT

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551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC  
601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA  
651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 1A (suite)

FIGURE 1B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN  
51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR  
101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL  
151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG  
201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q\*

FIGURE 2A  
-----

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC  
51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA  
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC  
151 TACACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA  
201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC  
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC  
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC  
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT  
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG  
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC  
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TCGGGCTCAA ATGGAAGAGT

551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC

601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 2A (suite)

FIGURE 2B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q\*

FIGURE 3A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC  
51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA  
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC  
151 TACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA  
201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC  
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC  
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC  
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT  
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG  
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC  
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TGCCGCTCAA ATGGAAGAGT

551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC  
601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA  
651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 3A (suite)



FIGURE 3B

1 MKLKTALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q\*

FIGURE 4A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC  
51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA  
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC  
151 TACACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA  
201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC  
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC  
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC  
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT  
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG  
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC  
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TCGGGCTCAA ATGGAAGAGT

551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC

601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 4A (suite)

FIGURE 4B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q\*

FIGURE 5A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC  
51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA  
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC  
151 TACACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA  
201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC  
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC  
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC  
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT  
401 TCGATGCGAT TGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG  
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC  
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TGCGGCTCAA ATGGAAGAGT

551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC

601 AAATACCAAG TTGAATTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 5A (suite)

FIGURE 5B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q\*

FIGURE 6A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC

51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA

101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC

151 TACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA

201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC

251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC

301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC

351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT

401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG

451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC

501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TCGGGCTCAA ATGGAAGAGT



551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC

601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 6A (suite)

FIGURE 6B

1 MKLKTALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q\*

FIGURE 7A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC  
51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA  
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC  
151 TACACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA  
201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC  
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC  
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC  
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT  
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG  
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC  
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TGCGGCTCAA ATGGAAGAGT

551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC  
601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA  
651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 7A (suite)

FIGURE 7B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN  
51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR  
101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL  
151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG  
201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q\*

FIGURE 8A

1 ATGAAACTGA AACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC  
51 CGCTTGTAGC AACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA  
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC  
151 TACACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA  
201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC  
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC  
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC  
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT  
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG  
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC  
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TGCGGCTCAÀ ATGGAAGAGT

551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC  
601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA  
651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 8A (suite)

FIGURE 8B

1 MKLKTALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN  
  
51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR  
  
101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL  
  
151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG  
  
201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q\*



FIGURE 9a

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC  
51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA  
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC  
151 TACACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA  
201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC  
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC  
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC  
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT  
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG  
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC  
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TGCGGCTCAA ATGGAAGAGT

551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC

601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCTGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 9A (suite)

FIGURE 9B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN  
51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR  
101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADDTL  
151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG  
201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q\*

FIGURE 10A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC  
51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA  
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC  
151 TACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA  
201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC  
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC  
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC  
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT  
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG  
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC  
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TCGGCTCAA ATGGAAGAGT

551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC

601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCTGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 10A (suite)

FIGURE 103

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN  
51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR  
101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL  
151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG  
201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q\*

FIGURE 11A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC  
51 CGCTTGTAGC AAACAGGCTG AAACCAGCGT TCCGGCAGAC AGCGTCCAAA  
101 GCAGCTCATC TGCTCCGGCA GCCCCAGCCC CATTGACCGA AGGCGTGAAC  
151 TACACTGTAT TGTCCACGCC TATCCCGCAA CAGCAGGCCG GCAAAGTCGA  
201 AGTCTTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC  
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC  
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC  
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT  
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG  
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC  
501 TGCATTTGAG GCTTCTGAAA GCCAAGCGCG TCGGCTCAA ATGGAAGAGT

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551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT CGTCGGCGGC  
601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA  
651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 11A (suite)



FIGURE 113

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SVQSSSSAPA APAPLTEGVN  
51 YTVLSTPIPQ QQAGKVEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR  
101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL  
151 KKWLSEQTAF DGKKVLAAFE ASESQARAAQ MEELTNKFQI SGTPTVIVGG  
201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q\*

FIGURE 12A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC  
51 CGCTTGTAGC AAACAGGCTG AAACCAGCGT TCCGGCAGAC AGCGTCCAAA  
101 GCAGCTCATC TGCTCCGGCA GCCCCAGCCC CATTGACCGA AGGCGTGAAC  
151 TACTGTAT TGTCCACGCC TATCCCGCAA CAGCAGGCCG GCAAAGTCGA  
201 AGTCTTGGA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC  
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC  
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC  
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT  
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG  
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC  
501 TGCATTTGAG GCTTCTGAAA GCCAAGCGCG TGCGGCTCAA ATGGAAGAGT

551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT CGTCGGCGGC

601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 12A (suite)

FIGURE 123

1 MKLKTALTS LTLLALAACS KQAETSVPAD SVQSSSSAPA APAPLTEGVN

51 YTVLSTPIPQ QQAGKVEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE ASESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q\*

FIGURE 13A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC  
51 CGCTTGTAGC AAACAGGCTG AAACCAGCGT TCCGGCAGAC AGCGTCCAAA  
101 GCAGCTCATC TGCTCCGGCA GCCCCAGCCC CATTGACCGA AGGCGTGAAC  
151 TACACTGTAT TGTCCACGCC TATCCCGCAA CAGCAGGCCG GCAAAGTCGA  
201 AGTCTTGGA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC  
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC  
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC  
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT  
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG  
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC  
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TCGGGCTCAA ATGGAAGAGT

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551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC

601 AAATACCAAG TTGAATTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 13A (suite)

FIGURE 13B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SVQSSSSAPA APAPLTEGVN

51 YTVLSTPIQ QQAGKVEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q\*

Figure 14A

1 GAGTATGCTC TTAGAGAAAA ATTGATCAAA AAAGCCAAAG GGAAAGGCCT  
51 ATTATCTTTA GATTGGGGCA GCCTGACCGA ACAAGAGGCA AGGCAGTTTA  
101 TCTATTTGAT TGAGAAAGAT CGATATTCTA ATCAATTGCT TGACCGATAT  
151 CAAAAAATC CAAGTAGTTT AAATAATCAA GAAAAAATA TTCTTGCATA  
201 TTTTATTAAC CAAACCTCTG GAGGTAACAC AGCTTGGGCA GCTTCGATAC  
251 TGAAAACGCC CCAGTCAATG GGTAATCTCA CTATTCCTTC CAAAGATATT  
301 AATAACACCT TATCGAAAGC CTATCAAACA TTGAGTCGTT ATGATTCTTT  
351 TGATTACAAA TCAGCTGTTG CCGCACAACC TGCACTTTAC TTATTAAACG  
401. GACCGCTTGG CTTCAGTGTC AAAGCAGCTA CTGTGGCAGC AGGAGGATAT  
451 AACATTGGAC AGGGAGCGAA AGCAATCTCT AATGGAGAAT ATCTGCATGG  
501 TACAGTTCAG GTTGTTAATG GCACATTGAT GGTTGCAGGA TCTGTATCTG  
551 CACAGGCTGC AATATCGGCC AAGCCTGCAC CTGTTACCCG TTATCTGAGC  
601 AATGACAGTG CTCCTGCTTT AAGACAAGCT TTAAGTCTG AAAGCCAGAG  
651 AATCCGCATG AAAGTCCGG AAGAGTATCG ACAAATAGGG AATCTTGCGA  
701 TAGCAAAAAT TGATGTTAAA GGATTACCGC AAAGGATGGA AGCATTTAGT



751 TCTTTCCAAA AAGGGGAACA TGGATTTATT TCGTTACCTG AAACAAAAAT  
801 TTTTAAACCT ATATCTGTTG ATAAATATCA TAATATTGCC TCTCCTCCTA  
851 GAGGAACATT AAGAAATATA GATGGAGAAT ATAAATTACT TGAAACTATA  
901 GCACAGCAAC TCGGAAATAA TCGTAATGTA TCAGGTAGAA TTGATCTATT  
951 TACAGAATTA AAGGCCTGTC AATCTTGCAG CAATGTTATT TTAGAGTTTA  
1001 GAAATCGCTA TCCAAATATT CAATTAAATA TTTTACAGG AAAATAG

**Figure 14A (suite)**

Figure 14B

1 EYALREKLIK KAKGKGLLSL DWGSLTEQEA RQFIYLIEKD RYSNQLLDRI  
51 QKNPSSLNNQ EKNILAYFIN QTSGGNTAWA ASILKTPQSM GNLTI PSKDI  
101 NNTLSKAYQT LSRYDSFDYK SAVAAQPALY LLNGPLGFSV KAATVAAGGY  
151 NIGQGAKAIS NGEYLHGT VQ VVNGTLMVAG SVSAQAAISA KPAPVTRYLS  
201 NDSAPALRQA LTAESQRIRM KLPEEYRQIG NLAIKIDVK GLPQRMEAFS  
251 SFQKGEHGFI SLPETKIFKP ISVDKYHNIA SPPRGTLRNI DGEYKLETI  
301 AQQLGNNRNV SGRIDLFTEL KACQSCSNVI LEFRNRY PNI QLNIFTGK

FIGURE 15A  
-----

1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC  
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG  
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC  
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT  
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA  
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC  
301 ATCGACGCCG CCTACGATAT GCGCGGCGAA AGCATTTTCC TCGCGGGCTT  
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC  
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT  
451 CCGTCCTCCG TGCTTTATGG GCGTACCAAC GCGGGCGGTG TCATCAACAT  
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT

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551 ATGGTTCGTG GGC AAACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTCACC GGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAA ACT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTA ACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT

FIGURE 15A (suite 1)

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1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG

1501 TCTTCCGCCG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC

1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

FIGURE 15A (suite 2)

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC  
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT  
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGC GTAACCG  
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG  
1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA  
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC  
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT  
2101 TACCGTTTCT GA

FIGURE 15A (suite 3)

FIGURE 15B  
-----

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL  
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG  
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG  
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL  
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD  
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND  
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSSNLT  
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG  
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT  
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGGYLSIDTL  
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN

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551 NPYIYAVSGK HRSRGVELSA IGQIPKKLY LRGSLGVMQA KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT

651 LPGFARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMPG NPRGYTARVN

701 YRF\*

FIGURE 15B (suite)



FIGURE 16A  
-----

1 ATGAAAATAT CATTTCA TTT AGCTTTATTA CCCACGCTGA TTATTGCTTC  
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG  
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC  
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT  
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA  
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC  
301 ATCGACGCCG CCTACGATAT GCGCGGCGAA AGCATTTTCC TCGCGGGCTT  
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC  
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT  
451 CCGTCCTCCG TGCTTTATGG GCGTACCAAC GGCGGCGGTG TCATCAACAT  
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT

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551 ATGGTTCGTG GGCAAACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCCG CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTGGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT

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1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAACATCT TCTCCGCCAC GCCCGATTTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG

1501 TCTTCCGCCG TGTTCACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC

1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAA ACTCTA TCTGCGCGGT

FIGURE 16A (suite 2)

1751 TCGTTGGGCG TGATGCAGGC GAAAGTCGTT GAAGACAAAG AAAATCCCGA  
1801 CCGAGTGGGC ATCCATTTGA ATAACACCAG CAACGTTACC GGCAACCTGT  
1851 TTTTCCGTTA TACCCCGACC GAAAACCTCT ACGGCGAAAT CGGCGTAACC  
1901 GGTACAGGCA AACGCTACGG TTACGACTCA AGAAATAAAG AAGTGACTAC  
1951 GCTTCCAGGC TTTGCCCGAG TTGATGCCAT GCTTGGCTGG AACCATAAAA  
2001 ATGTTAACGT TACCTTTGCC GCAGCCAATC TGTTCAATCA AAAATATTGG  
2051 CGTTCGGACT CTATGCCGGG TAATCCGCGC GGCTATACTG CCCGGGTAAA  
2101 TTACCGTTTC TGA

FIGURE 16A (suite 3)

FIGURE 16B  
-----

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL  
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG  
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG  
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL  
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD  
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND  
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSSNLT  
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG  
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT  
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL  
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN

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551 NPYIYAVSGK HRSRGVELSA IGQIIPKKTL SARFVGRDAG ESR\*RQRKSR  
601 PSGHPFE\*HQ QRYRQPVFPL YPDRKPLRRN RRNRYSQTLR LRLKK\*RSFY  
651 ASRLCPS\*CH AWLEP\*KC\*R YLCRSQSVQS KILAFGLYAG \*SARLYCPGK  
701 LPFL

FIGURE 16B (suite)

## FIGURE 17A

1 ATGAAAATAT CATTTCAATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC

51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG

101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC

151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT

201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA

251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC

301 ATCGACGCTG CCTACGATAT GCGCGGCGAA AGCATTTTCC TCGCGGTTTT

351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC

401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT TCTGAAAGGC

451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GCGGTGGCG TCATCAACAT

501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGAGCGGTTT

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551 ACGGCTCAAG GGCAAACCGC AGCCTGAATA TGGACATTAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATT

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCCG CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA TTTCACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACTTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC CTTAGGTTAC AGCCGCGCCT

FIGURE 17A (suite 1)



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1151 TTACTGCTTC CATCGATCCA TACGACCGAG CAAGCTGGCC GGCTTCGGGC

1201 AGATTGCAGC CTATCCTCAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAGTACAG CGGCCACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAACCCCG TTCACACACT TTACGCCTCG TATAACAAAG

1451 GTTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTCA

1501 TCTTCTGCCG TGTTTAACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTCAAA AGCAGTTGGC TGGACAATCG TTTGGACACC ACATTGTCCG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA CGCGGAAAAT

1651 AATCCCTACA CTTGGGCAGT CGGCGGCAAA CACCGTTCGC GTGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

FIGURE 17A (suite 2)

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAAA AAATCCCGAC  
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT  
1851 TTTCCGTTAT ACCCGACCGA AAACCTCTAC GGCGAAATCG GCGTAACCGG  
1901 TACAGGCAAA CGCTACGGTT ACAACTCAAG AAATAAAGAA GTGACTACGC  
1951 TTCCAGGCTT TGCCCGAGTT GATGCCATGC TTGGCTGGAA CCATAAAAAT  
2001 GTTAACGTTA CCTTTGCCGC AGCCAATCTG TTCAATCAAA AATATTGGCG  
2051 TTCGGACTCT ATGCCGGGTA ATCCGCGCGG CTATACTGCC CGGGTAAATT  
2101 ACCGTTTCTG A

FIGURE 17A (suite 3)

FIGURE 17B  
-----

1 MKISFHLALL PTLIIASFPV AAADTQDNGE IYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSRANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDFGL PYRMGFAHRN DFKDKKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSNFTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY SRAFTASIDP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KVLGGRYDK YTFNSENKLT

451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTS

501 SSAVFENADPE YTRQYETGVK SSWLDNRLDT TLSAYQIERF NIRYRPDAEN

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551 NPYTWAVGGK HRSRGVELSA IGQIPKKLY LRGS LGVMQA KVVEDKKNPD

601 RVGIHLNNTS NVTGNLFFRY TRPKTSTAKS A\*PVQANATV TTQEIKK\*LR

651 FQALPELMPC LAGTIKMLTL PLPQPICSIK NIGVRTLCRV IRAAILPG\*I

701 TVS

FIGURE 17B (suite)

FIGURE 18A  
-----

1 ATGAAAATAT CATTTTCA TTT AGCTTTATTA CCCACGCTGA TTATTGCTTC  
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG  
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC  
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT  
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA  
251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC  
301 ATCGACGCTG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGCGCGGTTT  
351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC  
401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC  
451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GCGGGCGGCG TCATCAACAT  
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGAGCGGTTT

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551 ACGGCTCATG GGCAAACCGC AGCCTGAATA TGGACATTAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACCT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT

FIGURE 18A (suite 1)

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1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC  
1201 AGATTGCAGC CTATTCTGAC CAAAACCGC CACAAAGCCG ACGCCTACGG  
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC  
1301 TCGGCGGTCTG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC  
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC  
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAATAAAG  
1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CAACACGTCTG  
1501 TCTTCGCCG TGTTC AACGC CGACCCCGAG TACACCCGCC AATACGAAAC  
1551 CGGTGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG  
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCGA CGAGCAAAAT  
1651 GATCCCTACA CTTGGGCAGT CGGCGGCAAA CACCGTTCGC GCGGCGTGGA  
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

FIGURE 13-A (suite 2)

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC  
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT  
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG  
1901 GTACAGGCAA ACGCTACGGT TACAACTCAA GAAATAAAGA AGTGACTACG  
1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA  
2001 TGTTAACATT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC  
2051 GTTCGGATGC CATGCCCCGGC GCGCCGCGCA CTTATACGGC GCGGGTTAAT  
2101 TACAGTTTCT AA

FIGURE 18A (suite 3)



FIGURE 18B  
-----

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL  
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG  
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG  
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL  
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD  
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND  
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSNLTL  
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG  
401 RLQPILTQNR HKADAYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT  
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAPYGG RGGYLSINTS  
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDEQN

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551 DPYTWAVGCK HRSRGVELSA IGQIIPKKLY LRGS LGVMQA KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT

651 LPGFARVDAM LGWNHKNVNI TFAAANLLNQ KYWRSDAMPG APRTYTARVN

701 YSF\*

FIGURE 18B (suite)

## FIGURE 19A

1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC  
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG  
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC  
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT  
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC TAGAAAAACA  
251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC  
301 ATCGACGCTG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGC GCGGTTT  
351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC  
401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC  
451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GGCGGCGGCG TCATCAACAT  
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGTGCGGTTT

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551 ACGGTTCTGTG GGCAAACCGC AGCCTGAATA TGGACATTAA CGAAGTGTTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACCT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCGGACTG CTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGCTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA TTTCACGCTA

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCATTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC CTTAGGTTAC AGCCGCGCCT

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1151 T TACTGCTTC CATCGATCCA TACGACCGAG CAAGCTGGCC GGCTTCGGGC  
1201 AGATTGCAGC CTATCCTCAC CCAAACCGC CACAAAGCCG ACTCCTACGG  
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC  
1301 TCGGCGGTCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC  
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC  
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAATAAAG  
1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CAACACGTCTG  
1501 TCTTCCGCCG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC  
1551 CGGTGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG  
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA CGAGCAAAAT  
1651 GATCCCTACA CTTGGGCAGT CGGCGGCAAA CACCGTTCGC GCGGCGTGGA  
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

FIGURE 19A (suite 2)

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC  
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT  
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG  
1901 GTACAGGCAA ACGCTACGGT TACAACTCAA GAAATAAAGA AGTGACTACG  
1951 CTTCCAGGCT TTGCCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA  
2001 TGTTAACATT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC  
2051 GTTCGGATGC CATGCCCGGC GCGCCGCGCA CTTATACGGC GCGGGTTAAT  
2101 TACAGTTTCT AA

FIGURE 19A (suite 3)

FIGURE 19B  
-----

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI \*KNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSSNFTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY SRAFTASIDP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT

451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGGYLSINTS

501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIIRYPDEQN

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551 DPYTWAVGGK HRSRGVELSA IGQIIPKKLY LRGSLGVMQA KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT

651 LPGFARVDAM LGWNHKNVNI TFAAANLLNQ KYWRSDAMPG APRTYTARVN

701 YSF\*

FIGURE 19B (suite)



FIGURE 20A

1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC  
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG  
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC  
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT  
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC TAGAAAAACA  
251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC  
301 ATCGACGCTG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGC GCGGTTT  
351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC  
401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC  
451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GCGGCGGGCG TCATCAACAT  
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGTGCGGTTT

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551 ACGGTTTCGTG GGCAAACCGC AGCCTGAATA TGGACATTAA CGAAGTGTTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACCT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCCG CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGCTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA TTTCACGCTA

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCATTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGCTAC CGCGGCAGTT

FIGURE 20A (suite I)

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1151 TCACCGTGCC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAACATCT TCTCCGCTAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAACAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAACCCAG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGTAT CGATACGTTG

1501 TCTTCCGCCG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACC ACATTGTCCG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCGA TCCAAAAAAC

1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

FIGURE 20A (suite 2)

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC  
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT  
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGC GTAACCG  
1901 GTACAGGCAA ACGCTACGGT TACA ACTCAA GAAATAAAGA AGTGACTACG  
1951 CTTCCAGGCT TTGCCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA  
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC  
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT  
2101 TACCGTTTCT GA

FIGURE 20A (Suite 3)

FIGURE 20B  
-----

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL  
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI \*KNKNYGTND LSSILEGNAG  
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG  
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL  
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD  
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND  
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLLSSNFTL  
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY RGSFTVPINP YDRASWPASG  
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT  
451 GNSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGGYLSIDTL  
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN

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551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGSLGVMQA KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT

651 LPGFARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMPG NPRGYTARVN

701 YRF\*

FIGURE 20B (suite)

## FIGURE 21A

1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC  
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG  
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC  
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT  
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA  
251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC  
301 ATCGACGCTG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGC GCGGTTT  
351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC  
401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC  
451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GGCGGCGGCG TCATCAACAT  
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGTGCGGTTT

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551 ACGGTTAGTG GGC AAACCGC AGCCTGAATA TGGACATTAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTCACC GGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAA ACT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCCGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT

1001 ACGCCTGGCA GCAGACTGAC AACAAAACCC TGTCGTCCAA TTTCACGCTA

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACTTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC CTTAGGTTAC AACCGCGCCT

FIGURE 21A (suite 1)



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1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG

1501 TCTTCCGCCG TGTTC AACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC

1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCTAA AAAACTCTAT CTGCGCGGTT

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC  
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT  
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG  
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG  
1951 CTTCCAGGCT TTGCCCAGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA  
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC  
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT  
2101 TACCGTTTCT GA

FIGURE 21A (suite 3)

FIGURE 21B  
-----

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL  
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG  
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG  
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYG\*WANR SLNMDINEVL  
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD  
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFKDKLQVW RSDLEYAFND  
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSNFTL  
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY NRAFSASINP YDRASWPASG  
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFMLGGRYDK YTFNSENKLT  
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL  
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRDPKPN

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551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGSLGVMQA KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT

651 LPGFARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMPG NPRGYTARVN

701 YRF\*

FIGURE 21B (suite)

## FIGURE 22A

1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC  
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG  
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC  
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT  
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA  
251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC  
301 ATCGACGCTG CCTACGATAT GCGCGGTGAA AGCATTTTCC TGCGCGGTTT  
351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC  
401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC  
451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GCGGCGGCG TCATCAACAT  
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGTGCGGTTT

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551 ACGGTTTCGTG GGCAAACCGC AGCCTGAATA TGGACATTAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACCT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGT CGCGAACACC GCAACCCGAC ATTGGGCTAC CGCGGCAGTT

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1151 TCACCGTGCC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAACATCT TCTCCGCTAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAACAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAACCCAG TCCACACACT TTATGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCTATT TGAGTATCGA CACTTCGTCT

1501 GCCGCCGTGT TCAACGCCGC CCCCAGGTAC ACTCGCCAAT ACGAAACCGG

1551 TGTGAAAAGC AGTTGGCTGG ACGACCGCCT CAGCACCACA TTGTCCGCCT

1601 ACCAAATCGA ACGCTTCAAT ATCCGCTACC GCCCGATCC AAAAAACAAC

1651 CCTTATATTT ATGCGGTTAG CGGCAAACAC CGTTCGCGCG GCGTGGAATT

1701 GTCCGCCATC GGGCAAATCA TCCCTAAAAA ACTCTATCTG CGCGGTTCGT

FIGURE 22.A (suite 2)

1751 TGGGCGTGAT GCAGGCGAAA GTCGTTGAAG ACAAAGAAAA TCCCGACCGA  
1801 GTGGGCATCC ATTTGAATAA CACCAGCAAC GTTACCGGCA ACCTGTTTTT  
1851 CCGTTATACC CCGACTGAAA ACCTCTACGG CGAAATCGGC GTAACCGGTA  
1901 CAGGCAAACG CTACGGCTAC AACTCAAGAA ATAAAGAAGT GACCACGCTT  
1951 CCAGGCTTTG CCCGAGTTGA TGCCATGCTC GGCTGGAACC ATAAAAATGT  
2001 TAACGTTACC TTTGCCGCTG CCAATCTGCT CAATCAAAAA TATTGGCGTT  
2051 CGGACTCTAT GCCGGGTAAT CCGCGCGGCT ATACTGCCCC GGTA AATTAC  
2101 CGTTTCTGA

FIGURE 22A (suite 3)



FIGURE 22B  
-----

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSNLTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY RGSFTVPINP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT

451 GNSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGYLSIDTSS

501 AAVFNAAPEY TRQYETGVKS SWLDDRLSTT LSAYQIERFN IRYRPDPKNN

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551 PYIYAVSGKH RSRGVELSAI GQIIPKKLYL RGSLGVMQAK VVEDKENPDR

601 VGIHLNNTSN VTGNLFFRYT PTENLYGEIG VTGTGKRYGY NSRNKEVTTL

651 PGFARVDAML GWNHKNVNVNVT FAAANLLNQK YWRSDSMPGN PRGYTARVNY

701 RF\*

FIGURE 22B (suite)

## FIGURE 23A

1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC  
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG  
101 CCACGCTACC TACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC  
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT  
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA  
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC  
301 ATCGACGCTG CCTACGATAT GCGCGGTGAA AGCATTTTCC TCGCGGTTT  
351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC  
401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC  
451 CCGTCTTCCG TGCTTTACGG CCGTACCAAC GGCGGCGGCG TCATCAACAT  
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGTGCGGTTT

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551 ACGGTTCTGT GGCAAACCGC AGCCTGAATA TGGACATTAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACCT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCCGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TCGAATACGC CTTCAACGAC

901 AAATGGCGCG CCCAATGGCA GCTCGCCAC CGCACGGCAG CGCAGGATTT

951 CGACCATTTT TATGCAGGCA GCGAAAACGG CAGCCGAATC AAACGCAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCTC TGTCGTCCAA CTTACGCTC

1051 AACGGCGACT ACACCATCGG TCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTEGGCTAC CGCGGCAGTT

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PCT/EP00/06943

1151 TCACCGTGCC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAAACATCT TCTCCGCTAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAACAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAACCCAG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGATATT TGAGTATCGA CACTTCGTCT

1501 GCCGCCGTGT TCAACGCCGC CCCCAGGTAC ACCCCCAATA CGAAACCGGC

1551 GTCAAAAGCA GTTGGCTGGA CAATCGTTTG GACACCACCC TGTCGGTTTA

1601 CCAAATCGAA CGCTTCAATA TCCGCTACCG CCCCAGTCCA AAAAACAACC

1651 CTTATATTTA TGCGGTTAGC GGCAAACACC GTTCGCGCGG CGTGGAATTG

1701 TCCGCCATCG GGCAAATCAT CCCCAAAAAA CTCTATCTGC GCGGTTTCGT

FIGURE 23A (suite 2)

1751 GGGCGTGATG CAGGCGAAAG TCGTTGAAGA CAAAGAAAAT CCCGACCGAG  
1801 TGGGCATCCA TTTGAATAAC ACCAGCAACG TTACCGGCAA CCTGTTTTTC  
1851 CGTTATACCC CGACCGAAAA CCTCTACGGC GAAATCGGCG TAACCGGTAC  
1901 GGGCAAACGC TACGGTTACA ACTCAAGAAA TAAAGAAGTG ACTACGCTTC  
1951 CAGGCTTTGC CCGAGTTGAT GCCATGCTTG GCTGGAACCA TAAAAATGTT  
2001 AACGTTACCT TTGCCGCAGC CAATCTGTTC AATCAAAAAT ATTGGCGTTC  
2051 GGA CTCTATG CCGGGTAATC CGCGCGGCTA TACTGCCCCG GTAAATTACC  
2101 GTTTCTGA

FIGURE 23A (suite 3)

FIGURE 23B  
-----

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL  
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG  
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG  
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL  
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD  
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHPN DFVKDKLQVW RSDLEYAFND  
301 KWRAQWQLAH RTAAQDFDHF YAGSENGSRI KRNYAWQQTD NKTLSNFTL  
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY RGSFTVPINP YDRASWPASG  
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFNSENKLT  
451 GNSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGAFAPYGG RGYLSIDTSS  
501 AAVFNAAPEY TPNTKPASKA VGWTIVWTPP CRFTKSNASI SATAPIQKTT

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551 LIFMRLAANT VRAAWNCPPS GKSSPKNSIC AVRWA\*CRRK SLKTKKIPTE

601 WASI\*ITPAT LPATCFVIP RPKTSTAKSA \*PVRANATVT TQEIKK\*LRF

651 QALPELMPCL AGTIKMLTLP LPQPICSIKN IGVRTLCLRVI RAAILPG\*IT

701 VS

FIGURE 23B (suite)



FIGURE 24A  
-----

1 ATGCAAATAC CATTTCAATTT GGCTTTATTA CCCACGCTGA TTATTGCTTC  
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG  
101 CCACGCTACC TACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC  
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT  
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA  
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC  
301 ATCGACGCCG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGCGCGGCTT  
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC  
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT  
451 CCGTCCTCCG TGCTTTATGG GCGTACCAAC GCGGCGGGTG TCATCAACAT  
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT

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551 ATGGTTCGTG GGCAAACCGT AGCCTGAATA TGGACATCAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATT

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCCG CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT

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1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG

1501 TCTTCCGCCG TGTTC AACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC

1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAA ACTCTA TCTGCGCGGT

FIGURE 24A (suite 2)

1751 TCGTTGGGCG TGATGCAGGC GAAAGTCGTT GAAGACAAAG AAAATCCCGA  
1801 CCGAGTGGGC ATCCATTTGA ATAACACCAG CAACGTTACC GGCAACCTGT  
1851 TTTTCCGTTA TACCCCGACC GAAAACCTCT ACGGCGAAAT CGGCGTAACC  
1901 GGTACAGGCA AACGCTACGG TTACGACTCA AGAAATAAAG AAGTGACTAC  
1951 GCTTCCAGGC TTGCCCCGAG TTGATGCCAT GCTTGGCTGG AACCATAAAA  
2001 ATGTTAACGT TACCTTTGCC GCAGCCAATC TGTTCAATCA AAAATATTGG  
2051 CGTTCGGACT CTATGCCGGG TAATCCGCGC GGCTATACTG CCCGGGTAAA  
2101 TTACCGTTTC TGA

FIGURE 24A (suite 3)

FIGURE 24B  
-----

1 MQIPFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL  
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG  
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG  
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL  
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD  
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFKDKLQVW RSDLEYAFND  
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSNLTL  
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG  
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT  
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL  
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN

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551 NPYIYAVSGK HRSRGVELSA IGQIIPKKTL SARFVGRDAG ESR\*RQRKSR

601 PSGHPFE\*HQ QRYRQPVFPL YPDRKPLRRN RRNRYRQTLR LRLKK\*RSY

651 ASRLCPS\*CH AWLEP\*KC\*R YLCRSQSVQS KILAFGLYAG \*SARLYCPGK

701 LPFL

FIGURE 24B (suite)

FIGURE 25A  
-----

1 ATGAAAATAT CATTTCAATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC  
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG  
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC  
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT  
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA  
251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC  
301 ATCGACGCTG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGC GCGGTTT  
351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC  
401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC  
451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GCGGCGGCG TCATCAACAT  
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGTGCGGTTT

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551 ACGGTTTCGTG GGC AAACCGC AGCCTGAATA TGGACATTAA CGAAGTGTTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATT A

701 CCGTCAAAC TCGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCA CGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCGGACTG CTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGCTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC T

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA TTTCACGCTA

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACC ACTTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC CTTAGGTTAC AGCCGCGCCT

FIGURE 25A (suite 1)



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1151 T TACTGCTTC CATCGATCCA TACGACCGAG CAAGCTGGCC GGCTTCGGGC

1201 AGATTGCAGC CTATCCTCAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTTG AAATTCGTCC

1301 TCGGCGGTCTG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAATAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CAACACGTCTG

1501 TCTTCCGCCG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGTGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA CGAGCAAAAT

1651 GATCCCTACA CTTGGGCAGT CGGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

FIGURE 25.A (suite 2)

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC  
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT  
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG  
1901 GTACAGGCAA ACGCTACGGT TACAACCTCAA GAAATAAAGA AGTGACTACG  
1951 CTTCCAGGCT TTGCCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA  
2001 TGTTAACATT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC  
2051 GTTCGGATGC CATGCCCCGGC GCGCCGCGCA CTTATACGGC GCGGGTTAAT  
2101 TACAGTTTCT AA

FIGURE 25A (suite 3)

FIGURE 25B  
-----

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSNFTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY SRAFTASIDP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT

451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSINTS

501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDEQN

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551 DPYTWAVGGK HRSRGVELSA IGQIPKKLY LRGSLGVMQA KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT

651 LPGFARVDAM LGWNHKNVNI TFAAANLLNQ KYWRSDAMPG APRTYTARVN

701 YSF\*

FIGURE 25B (suite)

## FIGURE 26.A

1 ATGAAAATAT CATTTCAATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC  
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG  
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC  
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT  
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA  
251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC  
301 ATCGACGCTG CCTACGATAT GCGCGGTGAA AGCATTTTCC TGC GCGGTTT  
351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC  
401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC  
451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GGCGGCGGCG TCATCAACAT  
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGAGCGGTTT

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551 ACGGCTCATG GGC~~CA~~AACCGC AGCCTGAATA TGGACATTAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATT

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTGGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT

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1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG

1501 TCTTCCGCCG TGTTC AACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC

1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

FIGURE 26.A (suite 2)

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC  
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT  
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGC GTAACCG  
1901 GTACAGGCAA ACGCTACGGT TACAACTCAA GAAATAAAGA AGTGACTACG  
1951 CTTCCAGGCT TTGCCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA  
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC  
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT  
2101 TACCGTTTCT GA

FIGURE 26A (suite 3)



## FIGURE 26B

1 MKISFHLALL PTLIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSNLTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT

451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL

501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN

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551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGS LGVMQA KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT

651 LPGFARVDAM LGWNHKNVNV TFAAANLLNQ KYWRSDSMPG NPRGYTARVN

701 YRF\*

FIGURE 26B (suite)

FIGURE 27A  
-----

1 MKRFTYTLSD GLCIEIELKR SAKKNLILRP VNMQTVSINV PPFFQDHALA

51 NWLAANETIL RNTLAKMPVH PVSHPNLPEW IWYRGIKTKL DTHSQSHIRI

101 TSSEILLPRK ETAAQIDHLR RLLNERAREY LLPRLEKHAA ETGLTPAATD

151 LSNAKTFWGV CRPHTGIRLN WRLIGTPEYV ADYVCIHELK HLRHPDHSPR

201 FWHLVNTLTP HTDNAKSWLK AHGRELFVLG \*

## FIGURE 27B

1 ATGAAACGCT TCACCTATAC TCTTCCGAC GGCTTGTGCA TCGAAATCGA

51 ACTCAAACGC AGTGCCAAGA AAAATCTGAT TCTGCGCCCC GTCAATATGC

101 AGACGGTCAG CATCAACGTC CCACCCTTTT TTCAAGACCA CGCGTTAGCA

151 AACTGGCTGG CGGCAAACGA AACGATTTTG CGGAACACGC TTGCTAAAAT

201 GCCCGTGCAT CCTGTTTCCC ACCCAAACCTT ACCCGAGTGG ATTTGGTATC

251 GGGGAATAAA GACCAAGCTG GATACCCACA GCCAAAGCCA TATCCGTATC

301 ACGTCGTCTG AAATCCTGCT TCCCCGAAAA GAAACCGCCG CACAAATCGA

351 CCACCTGCGC CGCCTGTTGA ACGAACGCGC CCGCGAATAC CTGCTGCCCC

401 GCCTTGAAAA ACACGCAGCC GAAACAGGAC TGA CTCCCGC TGCCACAGAC

451 CTGAGCAACG CAAAACCTT TTGGGGCGTA TGCCGCCCCG ACACCGGCAT

501 CCGCCTCAAC TGGCGGCTGA TCGGCACGCC CGAATACGTC GCCGACTATG

551 TCTGCATCCA CGAACTCTGC CACCTCCGCC ACCCCGACCA CAGTCCGCGC

601 TTTTGGCATT TGGTGAACAC GCTGACGCCG CATACCGACA ATGCTAAAAG

651 TTGGCTGAAG GCGCACGGGC GGAATTGTT TGTGCTGGGG TAA

FIGURE 27B (suite)

FIGURE 28A  
-----

1 ATGAGCAAGA TTATTGTGCT GACCGCAGGC CACAGCAACA CCGACCCGGG  
51 TCGGGTCAAC GGAAGCGACC GTGAGGCGGA CTTGGCGCAG GATATGCGCA  
101 ACATTGTGGC TTCAATCCTG CGTAACGATT ACGGCCTGAC CGTTAAAACC  
151 GACGGCACGG GCAAAGGCAA TATGCCGCTG CGCGAAGCGG TCAAGCTGAT  
201 TCGCGGCTCG GATGTGGCGA TTGAGTTTCA CACCAACGCT GCCGTCAGCA  
251 AAGCGGCGAC AGGCATCGAA GCCTTGAGTA CCGTTAAAAA CAAACGCTGG  
301 TGTCAGGTGT TGAGCAAAGC CGTTGCCAAG AAAACCGGCT GGAAACTGCG  
351 CGGCGAAGAC GGCTTTAAAC CCGACAATGC GGGCCAGCAT TCGCGCCTGG  
401 CTTATGCACA AGCCGGCGGC ATTGTGTTTG AGCCTTTTTT CATCAGCAAC  
451 GACACTGATT TGGCCTTGTT TAAGACGACT AAATGGGGCA TCTGCCGCGC  
501 GATTGCGGAC GCGATTGCGA TGGAATTGGG GCGGGCAAGA GTATGA

FIGURE 28B  
-----

1 MSKIIVLTAG HSNTDPGAVN GSDREADLAQ DMRNIVASIL RNDYGLTVKT  
51 DGTGKGNMPL REAVKLIRGS DVAIEFHTNA AVSKAATGIE ALSTVKNKRW  
101 CQVLSKAVAK KTGWKLRGED GFKPDNAGQH SRLAYAQAGG IVFEPFFISN  
151 DTDLALFKTT KWGICRAIAD AIAMELGAAR V\*

## FIGURE 29A

1 ATGCGTATTT TGGATATTTT TAAAAACCCA GCGACAGGCA ATGTGTCGCA

51 CTCGAAACTG TGGGCAAACG TTGCCTGCGC GCGGGGACG GTTAAGTTTG

101 TGATGCTGCC CGACCCGTCG GCGGAGATTT GGGCGGTGTA TTTGGGCATT

151 GTCGGCGGCT ATGCGGTGGC GCGTTCGTTG GTCAGCGTCA AACGTCAGGA

201 GGTCGAGAAT GAATCTCGTG AACTGCTGG CGAATAA



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FIGURE 29B  
-----

1 MRILDIFKNP ATGNVSHSKL WANVACAAGT VKFVMLPDPS AEIWAVYLG I

51 VGGYAVARSL VSVKRQEVEN ESRETAGE\*

FIGURE 30A

1 ATGCGGTGGC GCGTTCGTTG GTCAGCGTCA AACGTCAGGA GGTCGAGAAT  
51 GAATCTCGTG AAAGTCTGCTGG CGAATAACTG GCAACCGATT GCCATCATCG  
101 CGCTTGTCGG CACGGGTTTG GCGGTGTCGC ACCATCAAGG CTACAAGTCG  
151 GCTTTTGCGA AGCAGCAGGC GGTCATTGAG AAAATGAAGC GCGACAAGGC  
201 GCAAGCCCTG CTGTTGTCGG CTCAAAATA CGCCCGCGAA CTGGAACAGG  
251 CGCGTGCGGA AGCTAAAAAA TATGAAGTCA AGGCGCACGC CGTCGGCATG  
301 GCTTTGGCGA AAAAACAGGC GGAAGTCAGC CGTCTGAAAA CGGAAAATAA  
351 AAAGGAAATC GAAAATGTCC TTAAGTCAAGA CCGTAATAAT GCAGGCGGCG  
401 GTTGTATTGA CGGCTTTGGC CATCACGGCT TGCAGCTCTA CAAGCGCGCC  
451 CTCGGCTACG GAAATTAA

FIGURE 30B

1 MRWRVRWSAS NVRRSRMNLV KLLANNWQPI AIIALVGTGL AVSHHQGYKS

51 AFAKQQAVIE KMKRDKAQAL LLSAQNYARE LEQARAEAKK YEVKAHAVGM

101 ALAKKQAEVS RLKTENKKEI ENVLTQDRKN AGGGCIDGFG HHGLQLYKRA

151 LGYGN\*

FIGURE 31A  
-----

1 ATGTCCTTAC TCAAGACCGT AAAAATGCAG GCGGCGGTTG TATTGACGGC  
51 TTTGGCCATC ACGGCTTGCA GCTCTACAAG CGCGCCCTCG GCTACGGAAA  
101 TTAAGGTTGT CGAAAAGGCG GTCATGCCGA CACCGCCTGC CGCGTTGATG  
151 GTCGCGCCGG TCGCCCCGAA TCCGCCGAAA GACGGCAAGA CGGCCACGCT  
201 GTTGGAACAC GCCGCCGAGT TTGGCGGCTA TGTTGCCGAA CTTGAAAACC  
251 AAAATCAGGC TTGGCGCGAC TGGGCGGGCA ATCACTCCCG CAAAGTCGGA  
301 AACTGA

FIGURE 31B  
-----

1 MSLKTVKMQ AAVVLTALAI TACSSTSAPS ATEIKVVEKA VMPTPPAALM

51 VAPVRPNPPK DGKTATLLEH AAEEGGYVAE LENQNQAWRD WAGNHSRKVG

101 N\*

FIGURE 32A  
-----

1 GTGCTGGCAG TTTTGCTTGC TGGTGTAGCC TTCGCCCTGA GCGATGATTT  
51 CATGGTTGGC TGCTTTCAAA CGCCAACGGT ATTCGCCTTT TCGTCTTTA  
101 TAGATTTCAA AATACATAAG GTTTCTCCTA TGAATGAGTA CACGTTTTCT  
151 TACCGCTTTA ACGGCAAGTC CTGGTCATTG AGCATTTGGG CGGACAACCC  
201 TGAAGAAGCC AGGGCGAAAT TTCGGGCTGC ACGAGAAAAT GCGCACTATG  
251 ACGGCGAAGT TGTAGCAAAG GTTTATACAT TTGTAAATAT TTCGTGGGTT  
301 AAGAAATTGT ACAAGCGGAC AAAATATTTA ATGGGTATCA AAGAATGA

FIGURE 32B  
-----

1 VLAVLLAGVA FALSDDFMVG CFQTPTVFAF CVFIDFKIHK VSPMNEYTFS

51 YRFNGKSWSL SIWADNPPEEA RAKFRAAREN AHYDGEVVAK VYTFVNISWV

101 KKLYKRTKYL MGIKE\*

FIGURE 33A  
-----

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT  
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA  
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
201 GGCGCAGCAA CATTGGGCTG ATTTTCAAGC GTCCCATTA CAGCGTGATG  
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA  
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG



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551 AAAAAGAGGC TATGCCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

FIGURE 33A (suite 1)

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1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT  
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA  
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGGCAG GAAGTCGCCC  
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA  
1401 ATAA

FIGURE 33A (suite 2)

FIGURE 33B  
-----

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE\*

FIGURE 34A  
-----

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT  
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA  
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
201 GCGGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG  
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA  
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

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551 AAAAAGAGGC TTATGCCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

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1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT  
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA  
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC  
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA  
1401 ATAA

FIGURE 34A (suite 2)

FIGURE 34B  
-----

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE\*

## FIGURE 35A

1 ATGACATTGC TCAATCTAAT ATGCAAGATT ACGGTATTTT CGTTTGCCTG

51 AACTGACGC CCTATTTGCA ACATGAACTA TTTTCGGCTA TGAAATCCTA

101 TTTTCCAAA TATATCCTAC CCGTTTCACT TTTTACCTTG CCACTATCCC

151 TTTCCCATC CGTTTCGGCT TTTACGCTGC CTGAAGCATG GCGGGCGGCG

201 CAGCAACATT CGGCTGATTT TCAAGCGTCC CATTACCAGC GTGATGCAGT

251 GCGCGCACGG CAACAACAAG CCAAGGCCGC ATTCCTTCCC CATGTATCCG

301 CCAATGCCAG CTACCAGCGC CAGCCGCCAT CGATTTCTTC CACCCGCGAA

351 ACACAGGGAT GGAGCGTGCA GGTGGGACAA ACCTTATTTG ACTCTGCCAA

401 ATTTGCACAA TACCGCCAAA GCAGGTTCGA TACGCAGGCT GCAGAACAGC

451 GTTTCGATGC GGCACGCGAA GAATTGCTGT TGAAAGTTGC CGAAAGTTAT

501 TTCAACGTTT TACTCAGCCG AGACACCGTT GCCGCCCATG CGGCGGAAAA



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551 AGAGGCTTAT GCCCAGCAGG TAAGGCAGGC GCAGGCTTTA TTCAATAAAG

601 GTGCTGCCAC CGCGCTAGAT ATTCACGAAG CCAAAGCCGG TTACGACAAT

651 GCCCTGGCCC AAGAAATCGC CGTATTGGCT GAGAAACAAA CCTATGAAAA

701 CCAGTTGAAC GACTACACCG GCCTGGACAG CAAACAAATC GAGGCCATAG

751 ATACCGCCAA CCTGTTGGCA CGCTATCTGC CCAAGCTGGA ACGTTACAGT

801 CTGGATGAAT GGCAGCGCAT TGCCTTATCC AACAATCATG AATACCGGAT

851 GCAGCAGCTT GCCCTGCAAA GCAGCGGACA GGCCTTCGG GCAGCACAGA

901 ACAGCCGCTA TCCCACCGTT TCTGCCCATG TCGGCTATCA GAATAACCTC

951 TACACTTCAT CTGCGCAGAA TAATGACTAC CACTATCGGG GCAAAGGGAT

1001 GAGCGTCGGC GTACAGTTGA ATTTGCCGCT TTATACCGGC GGAGAATTGT

1051 CGGGCAAAAT CCATGAAGCC GAAGCGCAAT ACGGGGCTGC CGAAGCACAG

1101 CTGACCGCAA CCGAGCGGCA CATCAAACCTC GCCGTACGCC AGGCTTATAC

FIGURE 35A (suite 1)

1151 CGAAAGCGGT GCGGCGCGTT ACCAAATCAT GCGCAAGAA CGGGTTTTGG  
1201 AAAGCAGCCG TTGAAACTG AAATCGACCG AAACCGGCCA ACAATACGGC  
1251 ATCCGCAACC GGCTGGAAGT AATACGGGCG CGGCAGGAAG TCGCCCAAGC  
1301 AGAACAGAAA CTGGCTCAAG CACGGTATAA ATTCATGCTG GCTTATTTGC  
1351 GCTTGGTGAA AGAGAGCGGG TTAGGGTTGG AAACGGTATT TGCGGAATAA

FIGURE 35A (suite 2)

FIGURE 35B  
-----

1 MTLLNLICKI TVFPFA\*H\*R PICNMNYFRL \*NPIFPNISY PFHFLPCHYP

51 FPHPFRLLRC LKHGGRRSNI RLIFKRPITS VMQCAHGNNK PRPHSFPMYP

101 PMPATSASRH RFLPPAKHRD GACRWDKPYL TLPNLHNTAK AGSIRRLQNS

151 VSMRHAKNCC \*KLPKVISTF YSAETPLPPM RRKKRLMPSR \*GRRRLYSIK

201 VLPPR\*IFTK PKPVTTMPWP KKSPYWLRNK PMKTS\*TTTP AWTANKSRP\*

251 IPPTCWAHAIC PSWNVTVWMN GSALPYPTIM NTGCSSLPCK AADRRFGQHR

301 TAAIPPFLPM SAIRITSTLH LRRIMTTTIG AKG\*ASAYS\* ICRFIPAENC

351 RAKSMKPKRN TGLPKHS\*PQ PSGTSNSPYA RLIPKAVRRV TKS WRKNGFW

401 KAAV\*N\*NRP KPANNTASAT GWK\*YGRGRK SPKQNRNWLK HGINS CWLIC

451 AW\*KRAG\*GW KRYLRN

FIGURE 36A  
-----

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTTCG GCTATGAAAT  
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA  
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
201 GGCGCAGCAA CATTGGGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG  
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA  
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

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551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT  
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACATA  
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCAG GAAGTCGCCC  
1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA  
1401 ATAA

FIGURE 36A (suite 2)

FIGURE 36B

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE\*

FIGURE 37A  
-----

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT  
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA  
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
201 GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG  
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA  
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG



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551 AAAAAGAGGC TTATGCCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

FIGURE 37A (suite 1)

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1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC

1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 37A (suite 2)

## FIGURE 37B

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TOLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE\*

FIGURE 38A  
-----

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTTCG GCTATGAAAT  
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA  
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
201 GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG  
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA  
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

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551 AAAAAGAGGC TTATGCCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAAGT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCCGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

FIGURE 38A (suite 1)

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT  
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA  
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCAG GAAGTCGCCC  
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA  
1401 ATAA

FIGURE 38A (suite 2)

## FIGURE 38B

-----

1 MTLNLNMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDISKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE\*

FIGURE 39A

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTTCG GCTATGAAAT  
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA  
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
201 GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG  
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA  
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
451 CAGCGTTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG



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551 AAAAAGAGGC TATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAAGCTT

FIGURE 39A (suite 1)

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1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT  
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA  
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC  
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA  
1401 ATAA

FIGURE 39A (suite 2)

## FIGURE 39B

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEI AVLAEK QTYENQLNDY TDLD SKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVG YQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEÄQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE\*

## FIGURE 40 A

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT  
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTTTAC CTTGCCACTA  
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
201 GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG  
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA  
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

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551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

FIGURE 40A (suite 1)

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT  
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA  
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCAG GAAGTCGCCC  
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA  
1401 ATAA

FIGURE 40A (suite 2)

FIGURE 40B  
-----

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TOLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE\*

## FIGURE 41A

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT  
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA  
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
201 GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG  
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA  
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG



551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

FIGURE 41.A (suite 1)

WO 01/04150

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT  
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA  
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGGCAG GAAGTCGCCC  
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA  
1401 ATAA

FIGURE 41A (suite 2)

FIGURE 41B  
-----

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE\*

FIGURE 42A  
-----

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTCCGTTTG  
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT  
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTTAC CTTGCCACTA  
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
201 GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG  
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA  
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

WO 01/04150

PCT/EP00/06943

551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT  
601 AAAGGTGCTG CCACGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA  
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG  
701 AAAACCAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC  
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA  
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC  
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA  
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA  
951 CCTCTAACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG  
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA  
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC  
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

FIGURE 42A (suite 1)

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT  
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA  
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGGCAG GAAGTCGCCC  
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA  
1401 ATAA

FIGURE 42A (suite 2)

FIGURE 42B  
-----

1 MTLNLNMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDISKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE\*

FIGURE 43 A  
-----

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT  
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA  
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
201 GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG  
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA  
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG



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10/030740

551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

FIGURE 43A (suite 1)

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT  
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA  
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCAG GAAGTCGCCC  
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA  
1401 ATAA

FIGURE 43A (suite 2)

FIGURE 43B  
-----

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEI AVLAEK QTYENQLNDY TDLSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVG YQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE\*

FIGURE 44A  
-----

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT  
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA  
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
201 GGCAGCAGCAA CATTGGCTG ATTTTCAAGC GTCCATTAC CAGCGTGATG  
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA  
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

FIGURE 44A (suite 1)

FIGURE 44B  
-----

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEÄQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE\*

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGT  
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA  
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGGCAG GAAGTCGCCC  
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA  
1401 ATAA

FIGURE 44B (suite)

FIGURE 45A  
-----

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT  
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA  
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
201 GGCGCAGCAA CATTGCGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG  
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA  
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG



551 AAAAAGAGGC TTATGCCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

FIGURE 45A (suite 1)

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCAG GAAGTCGCCC

1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 45A (suite 2)

FIGURE 45 B  
-----

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

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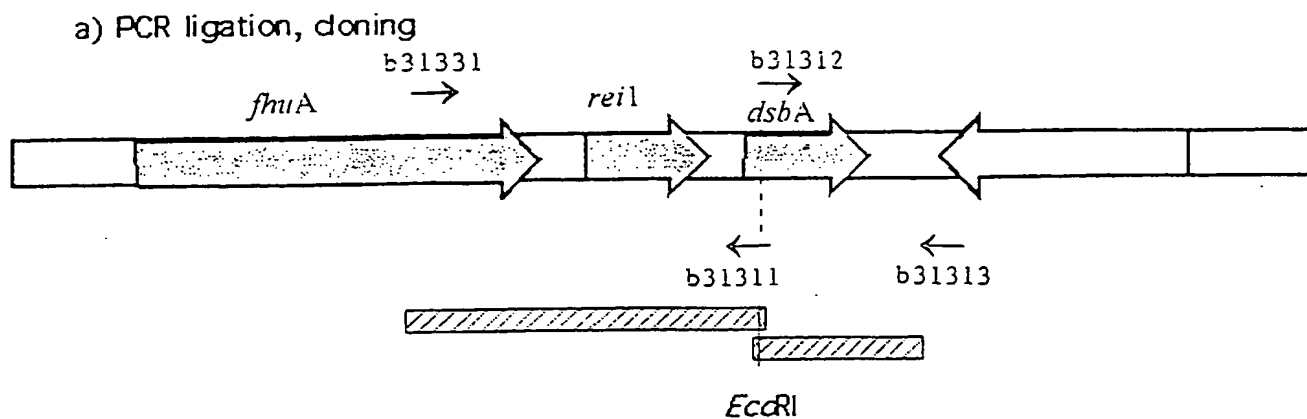
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYYNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

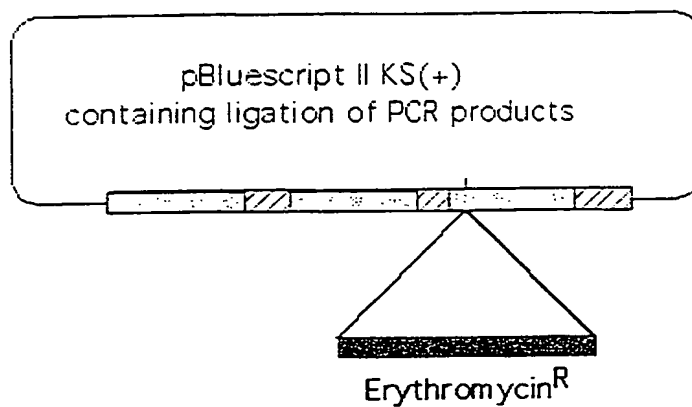
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE\*



b) Insertion of erythromycin resistance cassette



c) Transformation of *Nm* to erythromycin resistance and DsbA1<sup>-</sup>

Figure 46

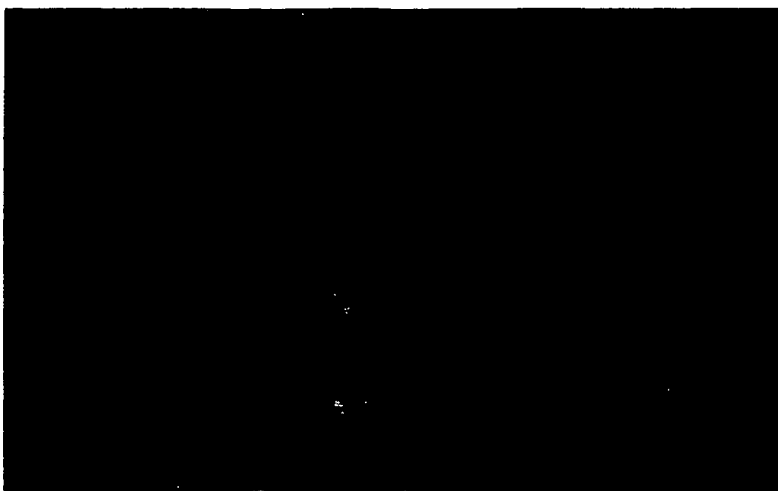


Figure 47A

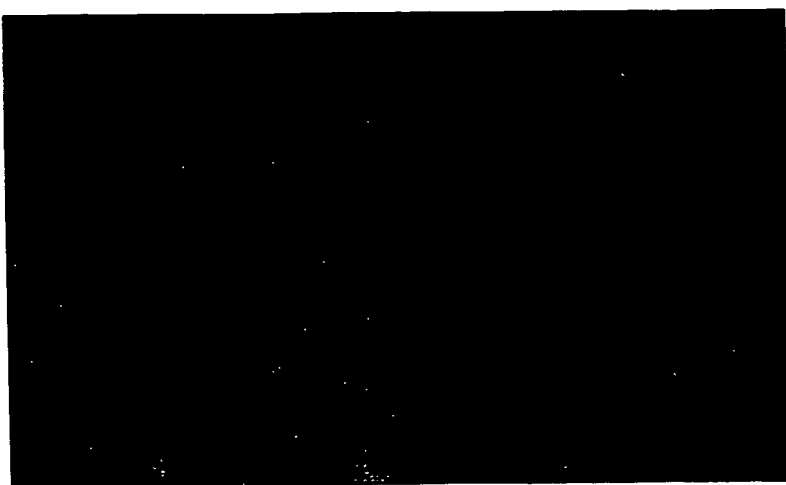


Figure 47B

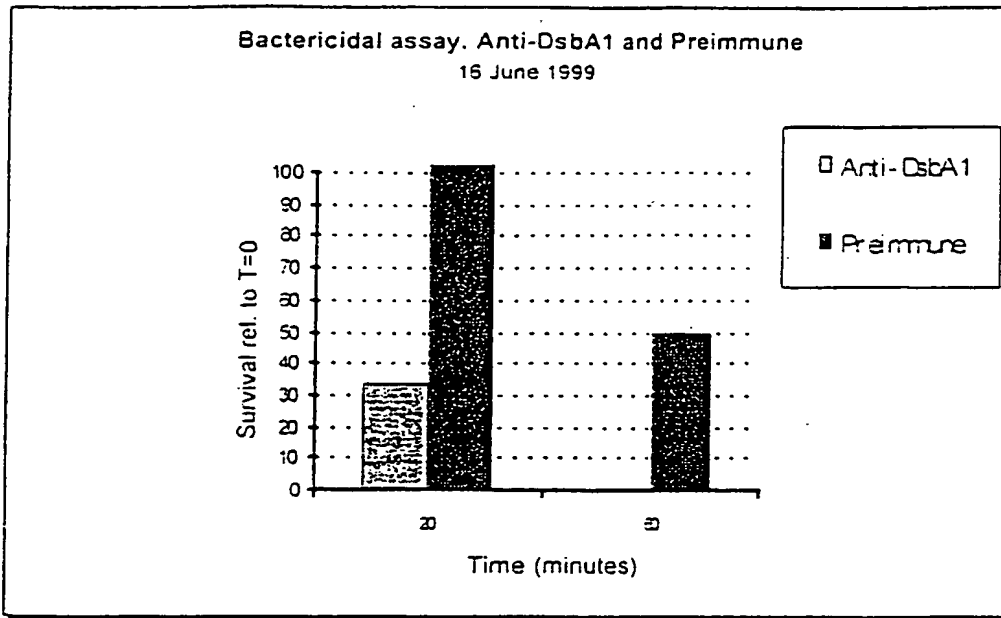


Figure 48

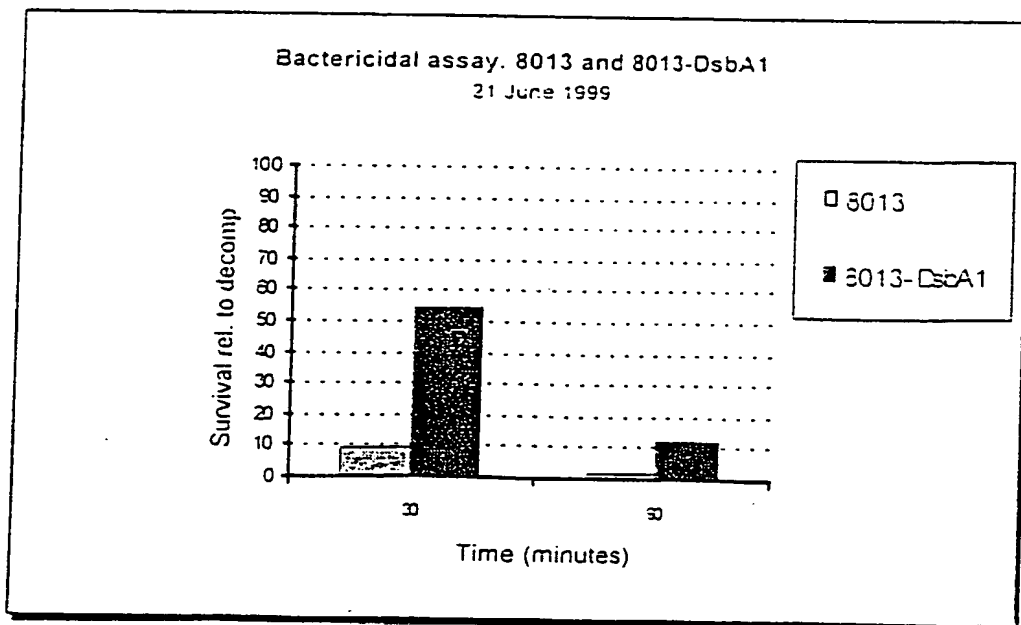


Figure 49

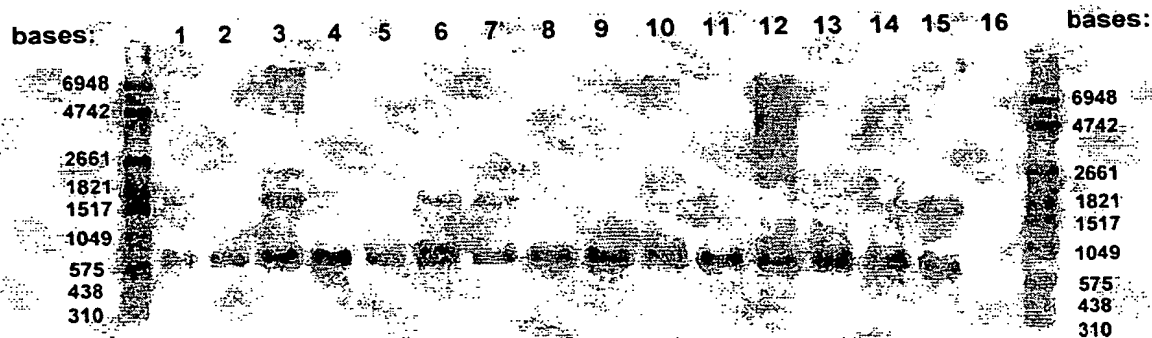


Figure 50